Trying to stay warm.

PHYSIOLOGY

Pigs in Blankets

Human infants, like other newborn animals and hibernating rodents, are endowed with a built-in central heating system: Mitochondrial proton gradients are uncoupled from ATP production in brown adipose tissue, so chemical energy is converted directly into heat, which protects against the vicissitudes of an uncertain environment. Uncoupling protein 1 (UCP1), which is present only in brown adipose tissue, is critical for thermogenesis. Piglets, though, are unusual in this regard, as they lack this kind of fat and rely instead on shivering as a way to stay warm.

Berg *et al.* looked for and, surprisingly, found *UCP1* sequences in preliminary pig genome data. But closer examination revealed that the gene is peppered with small errors and is missing exons 3 to 5, a deletion that they also found in other species of pig, wild boar, and hog, and that almost certainly renders the gene useless. The pig *UCP1* sequences have randomly drifted away from those of other closely related animals, further evidence that the gene is nonfunctional and that this drift has been going on for some 20 million years, implying that the gene has been out of commission for the same period. Many pig species hail from relatively balmy environments, where such a heat-generating system would not have been needed for survival. Not so for the wild boar, which thrives in colder climes, partly because of the evolution of a nest-building behavior that compensates for the ancient loss of *UCP1* and brown adipose tissue. — GR

PLoS Genet. **2**, e129 (2006).

MICROBIOLOGY

Pleiotropic Tensegrity

Systems biology has popularized the view of metabolic and regulatory pathways as networks, and experimental and bioinformatics studies of protein-protein interactions have codified these networks as centralized hubs and radiating spokes. One somewhat deceptive implication inherent in these representations is the static character of these linkages.

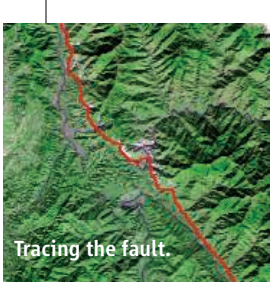
Knight *et al.* provide a comprehensive proteomic analysis of *Pseudomonas fluorescens* SBW25, where spontaneous adaptive mutations in the *wspF* gene result in the ability to grow at the air/liquid interface (as opposed to within broth). Although the genetic difference between the parental SM (smooth morphology) and evolved LSWS (Large Spreading Wrinkly Spreader) strains corresponds to the replacement of a serine with an arginine in a single component of the Wsp chemotaxis pathway, there are significant differences in the amounts of 46 proteins (identified by mass spectrometry and recourse to the draft genome), primarily with functions in amino acid uptake and catabolism. Mapping the variation in the amounts of these proteins across independent replicate cultures revealed that the LSWS strain, in comparison to the original SM strain, exhibits a distinct network of covariation. These distributed, yet coordinated, changes in protein levels suggest that understanding network dynamics will be key to explaining pleiotropy. — GJC

Nat. Genet. **38**, 10.1038/ng1867 (2006).

GEOPHYSICS

The Big Dig

By analyzing aerial photographs of the M_w 7.6 Kashmir earthquake that struck northern Pakistan on 8 October 2005, Avouac *et al.* show that, unusually for this area, the rupture broke through to the surface. Displacements are evident in ASTER images of the region taken just weeks after the event when these are compared to images of the same area from 5 years earlier. The surface rupture was confined to a strip a few hundred meters wide. Horizontal slip along the fault measured ~4 m on average, but offsets as large as 7 m were seen north of Muzaffarabad. Because the earthquake was shallow and compact, it caused intense but localized destruction. This pronounced movement along the fault suggests that adjacent regions may be soon be prone to large earthquakes. — JB



Tracing the fault.

Earth Planet. Sci. Lett. 10.1016/j.epsl.2006.06.025 (2006).

MICROBIOLOGY

More A's than B's

In contrast to eukaryotes and bacteria, archaea have only recently become the objects of study, and then primarily as hardy denizens of extreme environments, such as hot springs or acid mines. However, as analytical techniques for detecting trace amounts of archaeal components in unpurified samples have been refined and more widely applied, evidence has been accumulating that these species are likely to participate in biogeochemical cycles that affect all spheres of life.

Wuchter *et al.* and Leininger *et al.* have looked at the archaea-based oxidation of ammonia in North Sea waters and in northern European soil, respectively. They have measured the amounts of the gene encoding ammonia monooxygenase, the first enzyme in the nitrification pathway, and correlated these data with the presence of Crenarchaeota-specific lipids. Quantitation of ammonia monooxygenase genes in the upper 1000 m of the North Atlantic and across pristine and fertilized soils revealed that the archaeal version was generally several orders of magnitude more abundant than the bacterial enzyme. Incubation of the marine sample and estimates of the rates of Crenarchaea growth and production of nitrite yielded an oxidation flux of about 3 fmol of

Continued on page 1205

Continued from page 1203

NH_3 per cell per day, which could be extrapolated to a global inorganic carbon fixation rate of 4 x 10^{13} mol of C per year. — GJC

Proc. Natl. Acad. Sci. U.S.A. 103, 12317 (2006); *Nat.* **442**, 806 (2006).

MATERIALS SCIENCE

Mining for Crystals

Predicting the crystal structure of an alloy is challenging, because even small changes in composition can lead to large changes in the way the atoms prefer to coordinate. Fischer *et al.* have developed a technique that mines the existing crystal database to determine top candidate structures, which are then evaluated using quantum mechanical calculations. The model determines correlations for structural motifs that jointly appear in a single alloy system at different compositions, and thereby assigns probabilities to candidate structures, given those already known in the system. In one test, the authors considered the Ag-Mg alloy with 75% Mg content, for which the exact crystal structure is undetermined. The top candidate highlighted by their model was the $Cu_{2.82}P$ structure, an uncommon motif that nonetheless was computed to have the lowest ground-state energy.

They also tested the model by selectively removing specific compositions from the database to see if the remaining data could be successfully used to predict the correct structures; this approach succeeded 90% of the time in placing the true missing structure among the top five candidates. — MSL

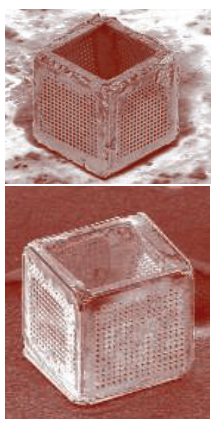
Nat. Mater. **5**, 641 (2006).

CHEMISTRY

Microscale Origami

Recent advances in lithography and other surface-patterning techniques have fostered construction of a wide range of microfluidic devices that offer precise control over chemical and biochemical reactions and separations at or below microliter volume scales. However, one limitation of this fabrication technology is its inherent restriction to two-dimensional device geometries.

Leong *et al.* overcome this limitation by patterning flat wafers with solder deposited along hinge lines. When heat is applied to melt the solder, the wafers fold spontaneously along the hinges to form cubic or pyramidal boxes, with volumes ranging from ~0.2 to 8 nl. The authors use photolithography to imprint distinct pore arrangements into the surfaces set to become the box faces. As a result, they can inject chemical reagents embedded in polymeric gels and control the rate and orientation of their release. The fabrication process is high-yielding, and when nickel is used as the substrate, the corresponding box can be manipulated with an external magnet to release its chemical cargo in a spatially selective manner. — JSY



Nanoliter boxes.

J. Am. Chem. Soc. **128**, 10.1021/ja063100z (2006).

CREDIT: LEONG *ET AL.*, *J. AM. CHEM. SOC.* **128**, 10.1021/JA063100Z (2006)

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<< Waking Stem Cells

Hematopoietic stem cells (HSCs) reside in bone marrow in a nondividing state from which they can be roused to enter the cell cycle. Noting the similarity of HSC dormancy to mammalian hibernation and *Caenorhabditis elegans* dauer formation, Yamazaki *et al*. looked at the PI3K (phosphatidylinositol 3-kinase)–Akt–FOXO signaling pathway. In quiescent cells freshly isolated from mouse bone marrow, no phosphorylated (activated) Akt was apparent and its downstream target FOXO3a was found in the nucleus; in contrast, phosphorylated Akt and FOXO3a were found in the cytoplasm of cycling progenitor cells. Cytokine treatment of quiescent cells led to polarization of the lipid raft marker GM1 ganglioside as well as phosphorylation of Akt and relocation of FOXO3a to the cytoplasm. Depleting cholesterol with β-cyclodextrin (MβCD) in order to inhibit lipid raft clustering suppressed Akt activation and FOXO3a relocation. When single HSCs that had survived without dividing for several days in the presence of MβCD, stem cell factor, and thrombopoietin were placed in MβCD-free medium, they proliferated and differentiated along various myeloid lineages in vitro and could repopulate the hematopoietic system of lethally irradiated mice. Thus, lipid raft clustering may mediate HSC emergence from dormancy via signaling pathways resembling those involved in the dauer stage. — EMA

EMBO J. **25**, 3515 (2006).

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